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Research Article

Two new arthroconidial yeast species from bark and pit mud in China

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Abstract

A study on yeast species from the genera *Geotrichum* and *Magnusiomyces* in southwest and central China was conducted based on morphological and molecular phylogenetic analyses using the ITS region and the D1/D2 domain of the LSU rRNA gene. The research identified two new yeast species: *Geotrichum hubeiense* and *Magnusiomyces pitmudophilus*. The study contributed to understanding arthroconidial yeast diversity in fermentation and natural environments and paved the way for future taxonomic and ecological studies. Descriptions, illustrations, and phylogenetic analysis results of the two new taxa are provided.

Key words: Arthroconidial yeast, *Geotrichum*, *Magnusiomyces*, two new species

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Introduction

The ascomycetous yeasts, or fungi that exhibit yeast-like characteristics and form arthroconidia, are categorized under the genera *Geotrichum* and *Magnusiomyces* (de Hoog and Smith 2004, 2011a, 2011b, 2011c, 2011d, 2011e; Zhu et al. 2024b). These fungi are ubiquitous and are frequently found in association with dairy products (Marcellino et al. 2001; Banjara et al. 2015), Chinese Baijiu production (Zhu et al. 2024b), marine environments (Zhu et al. 2024b), cosmetics (Kataoka et al. 2013; Takei et al. 2015), human infection (Ersoz et al. 2004; Özkaya-Parlakay et al. 2012; Fasciana et al. 2017; Shah and Mauger 2017; Tanuskova et al. 2017; Keene et al. 2019; Erman et al. 2020; Flateau et al. 2021; Tshisevhe et al. 2021; Noster et al. 2022), and plant rot (Vadkertiová et al. 2012; Gao et al. 2020; Wang et al. 2022), as well as in the emerging new energy industry (Kurylenko et al. 2020).

Early molecular phylogenetic studies utilizing sequence analyses of the LSU (Kurtzman and Robnett 1995), SSU (Ueda-Nishimura and Mikata 2000), and ITS rDNA sequences (de Hoog and Smith 2004) classified two distinct groups of arthroconidial yeasts, including the sexual genera *Dipodascus*, *Galactomyces*,

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and *Magnusiomyces*, and the asexual genera *Geotrichum* and *Saprochaete*. de Hoog and Smith (2004) further confirmed these groups through phylogenetic analyses of the ITS region and DNA/DNA reassociation data, validating the existence of Ribosomal Groups 1 and 2 among arthroconidial yeasts or yeast fungi in Hemiascomycetes. According to the nomenclature code adopting the "one fungus, one name" principle (McNeill et al. 2012), Zhu et al. (2024b) revised these two monophyletic groups as *Geotrichum* and *Magnusiomyces* based on the sequences of the internal transcribed spacer (ITS) region and the D1/D2 domain of the large subunit of the rDNA gene and recognised 28 species in the genus *Geotrichum* and 17 species in the genus *Magnusiomyces*. Subsequently, *Geotrichum pandrosioniae*, isolated from the dung of *Vombatus ursinus*, and *Dipodascus hypatia* isolated from soil under *Zingiber zerumbet*, were described by Tan and Shivas (2023) from Australia. *Geotrichum enheduannae* from the scat of *Casuarius casuarius* was also described by Tan and Shivas (2024) from Australia.

China, known for its rich biodiversity, is one of the most biodiverse countries in the world. (The Biodiversity Committee of Chinese Academy of Sciences, 2024). However, compared to the extensive studies on plants and animals, fungal diversity, particularly yeasts, has received significantly less attention. The 'Catalogue of Life China: 2024 Annual Checklist' documents a comprehensive count of 69,407 species within the Animalia kingdom, 39,897 species within the Plantae kingdom, and 26,591 species within the Fungi kingdom. Boekhout et al. (2022) reported that at least 782 yeast species were known in China by 2020, and 125 new yeast species were discovered in the subsequent four years (Gao et al. 2021; Liu et al. 2021, 2023, 2024c, 2024a, 2024b; Shi et al. 2021; Chai et al. 2022b, 2022c, 2022a, 2023, 2024; Chu et al. 2022; Hu et al. 2022; Wei et al. 2022, 2024a, 2024b; Qiao et al. 2023, 2024; Yu et al. 2023; Zhu et al. 2023a, 2023b, 2024b, 2024a; Cai et al. 2024; Guo et al. 2024a, 2024b; Jiang et al. 2024; Lu et al. 2024; Xi et al. 2024). Furthermore, based on DNA metabarcoding analyses, they estimated that the natural world likely hosts over 20,000 yeast species. This suggests that many yeast species remain to be discovered, highlighting the vast potential for future exploration in this field.

During our surveys of yeast diversity in samples from traditional fermentation and terrestrial natural environments, five isolates representing two arthroconidial yeast species in *Geotrichum* and *Magnusiomyces* were identified based on morphology and molecular phylogenetic analyses, which increased the species diversity of arthroconidial yeast species in China.

Materials and methods

Sample collection and yeast isolation

Twenty traditional fermentation environment samples and nine terrestrial natural environment samples were collected, and important collection information was noted (Rathnayaka et al. 2024) from southwest China, namely, Guizhou Province, in May 2023, and central China, namely, Hubei Province, in July 2023, respectively. All samples were placed into sterile sampling bags, transferred to the laboratory at 25 ± 2 °C, and subjected to yeast isolation. The pit mud samples, containing rich microbial communities used in the traditional Chinese

Baijiu brewing process, were processed by suspending 60 grams in a 250 mL conical flask containing 180 mL of sterile water and shaking at 200 rpm for 30 minutes at 30 °C. Subsequently, each suspension was diluted to 1×10^{-1}, and 100 µL of stock and dilution was plated on yeast extract peptone dextrose agar (YPD, w/v, 2% glucose, 1% yeast extract, 2% peptone, and 2% agar) plates supplemented with 200 µg/mL chloramphenicol. Plates were incubated at 30 °C for 3–5 days. The moss-covered bark samples from unknown plants were enriched and isolated using the method described by Zhu et al. (2023c). Yeast and yeast-like colonies on the plates were picked, purified, and preserved in 25% glycerol at −80 °C.

Phenotypic characterization

Morphological characteristics and physiological and biochemical properties were examined according to standard methods described by Kurtzman et al. (2011). The assimilation of carbon and nitrogen compounds was conducted in liquid media. The potential sexual cycles of strains representing new species were investigated using corn meal agar (CMA, w/v, 2.5% corn starch and 2% agar), potato dextrose agar (PDA, w/v, 20% potato infusion, 2% glucose, and 2% agar), yeast extract–malt extract agar (YM, w/v, 1% glucose, 0.3% yeast extract, 0.3% malt extract, 0.5% peptone, and 2% agar), V8 agar (w/v, 10% V8 juice and 2% agar), and yeast carbon base agar (YCB, w/v, 1.17% yeast carbon base and 2% agar). A loopful of cells of each test strain was inoculated separately or mixed on agar plates, incubated at 25 °C for up to two months, and examined periodically.

DNA extraction, sequencing, and phylogenetic analyses

A sesame seed-sized quantity of fresh yeast cells was transferred to 70 µL of sterile 0.1 M sodium hydroxide solution, where they were subjected to lysis at 98 °C for 15 minutes to extract yeast genomic DNA. The ITS region and D1/D2 domain of the LSU rRNA gene were amplified using primers ITS1 and ITS4 (White et al. 1990) and NL1 and NL4 (O'Donnell 1993), respectively, and were also sequenced using the methods described by Bai et al. (2002). Sequence alignments were conducted with MAFFT v.7 (Katoh and Standley 2013), with ambiguous positions excluded using GBLOCKS v.0.91b (Castresana 2000). Phylogenetic analysis based on single ITS or D1/D2 sequences was executed utilizing the Neighbor-Joining model in MEGA v.7 with evolutionary distances derived from Kimura's two-parameter model (Kimura 1980; Kumar et al. 2016; Lachance 2022). Bootstrap analyses were performed on 1,000 random re-sampling (Felsenstein 1985). Maximum parsimony (MP), Bayesian Inference (BI), and maximum likelihood (ML) analyses were conducted on the combined ITS and D1/D2 sequences using PAUP v.4.0b10 (Swofford 2003), MRBAYES v.3.2 with 1,000,000 generations (Ronquist et al. 2012), and RAXML-HPC 7.2.8 with 1,000 bootstrap replicates (Stamatakis 2006), respectively. The optimal nucleotide substitution model was estimated using MODELTEST v.3.04 (Posada and Crandall 1998), with the GTR + I + G model selected for the ML and BI analyses.

Results

Phylogenetic analyses

A total of five yeast strains from pit mud and bark samples were preliminarily identified as two novel arthroconidial yeast species in the genera *Geotrichum* and *Magnusiomyces* using the BLAST search tool based on the ITS and D1/D2 sequences against the NCBI GenBank database. Besides the newly generated sequences, additional related sequences (Suppl. material 3) were also downloaded from GenBank for the phylogenetic analyses.

Strains 2-25-ESXF-26-2 and 2-17-ESXF-26-1^T from the same bark samples in Hubei province possessed identical ITS sequences and similar D1/D2 sequences with one nucleotide substitution, indicating that they were conspecific. The phylogenetic analyses based on the D1/D2 and ITS sequences confirmed the affinity of the 2-17-ESXF-26-1^T group to the genus *Geotrichum* with high bootstrap support (Fig. 1, Suppl. materials 1, 2). However, the phylogenetic position of this group within the genus was not consistently resolved when the combined ITS and D1/D2 sequences and single ITS or D1/D2 sequences were used (Fig. 1, Suppl. materials 1, 2). The 2-17-ESXF-26-1^T group was closely related to *Dipodascus hypatia* in the *Geotrichum* clade in the tree based on the D1/D2 sequences (Suppl. material 1) but exhibited a close relationship with *G. carabidarum*, *G. histeridarum*, and *Dipodascus hypatia* in the ITS tree (Suppl. material 2). The bootstrap support for the phylogenetic relationships of the 2-17-ESXF-26-1^T group with the described species of the genus *Geotrichum* was lower than 70% in the ITS tree (Suppl. material 2) but 100% in the D1/D2 tree (Suppl. material 1). The results of pairwise comparisons indicated that strain 2-17-ESXF-26-1^T exhibited 84 (15.2%, 67 substitutions and 17 gaps, total length: 552) nucleotide differences and 37 (14.0%, 23 substitutions and 14 gaps, total length: 265) nucleotide differences from its closely related species *Dipodascus hypatia* in the D1/D2 domain and ITS region, respectively. Strain 2-17-ESXF-26-1^T possessed 86 (16.1%, 58 substitutions and 28 gaps, total length: 533) nucleotide differences and 38 (15.8%, 22 substitutions and 16 gaps, total length: 241) nucleotide differences from its closely related species *Geotrichum histeridarum* in the D1/D2 domain and ITS region, respectively. Strain 2-17-ESXF-26-1^T possessed 95 (17.2%, 58 substitutions and 37 gaps, total length: 553) nucleotide differences and 38 (14.4%, 24 substitutions and 14 gaps, total length: 264) nucleotide differences from its closely related species *Geotrichum carabidarum* in the D1/D2 domain and ITS region, respectively. The results indicated that the 2-17-ESXF-26-1^T group represents a novel species of the genus *Geotrichum*, for which the name *G. hubeiense* is proposed.

Strains 735-8, 735-10, and 682-Y-2^T, isolated from two pit mud samples collected from different brewing workshops of a well-known Chinese Baijiu enterprise in Zunyi City, Guizhou Province, possessed identical ITS and D1/D2 sequences, thus suggesting their conspecificity. Strains 735-8 and 735-10 were isolated from one workshop, while strain 682-Y-2^T was isolated from another. In the combined D1/D2 and ITS tree and the single ITS tree, the group 682-Y-2 and other six species, namely, *Magnusiomyces fungicola*, *M. gigas*, *M. japonica*, *M. magnusii*, *M. suaveolens*, and *M. tetraspermus*, grouped in a branch in the genus *Magnusiomyces* (Fig. 1, Suppl. material 2). However, in the D1/D2 tree, the aforementioned branch newly added the species *M. saccharophilus* besides the six species (Suppl. material 1). The phylogenetic positions of the

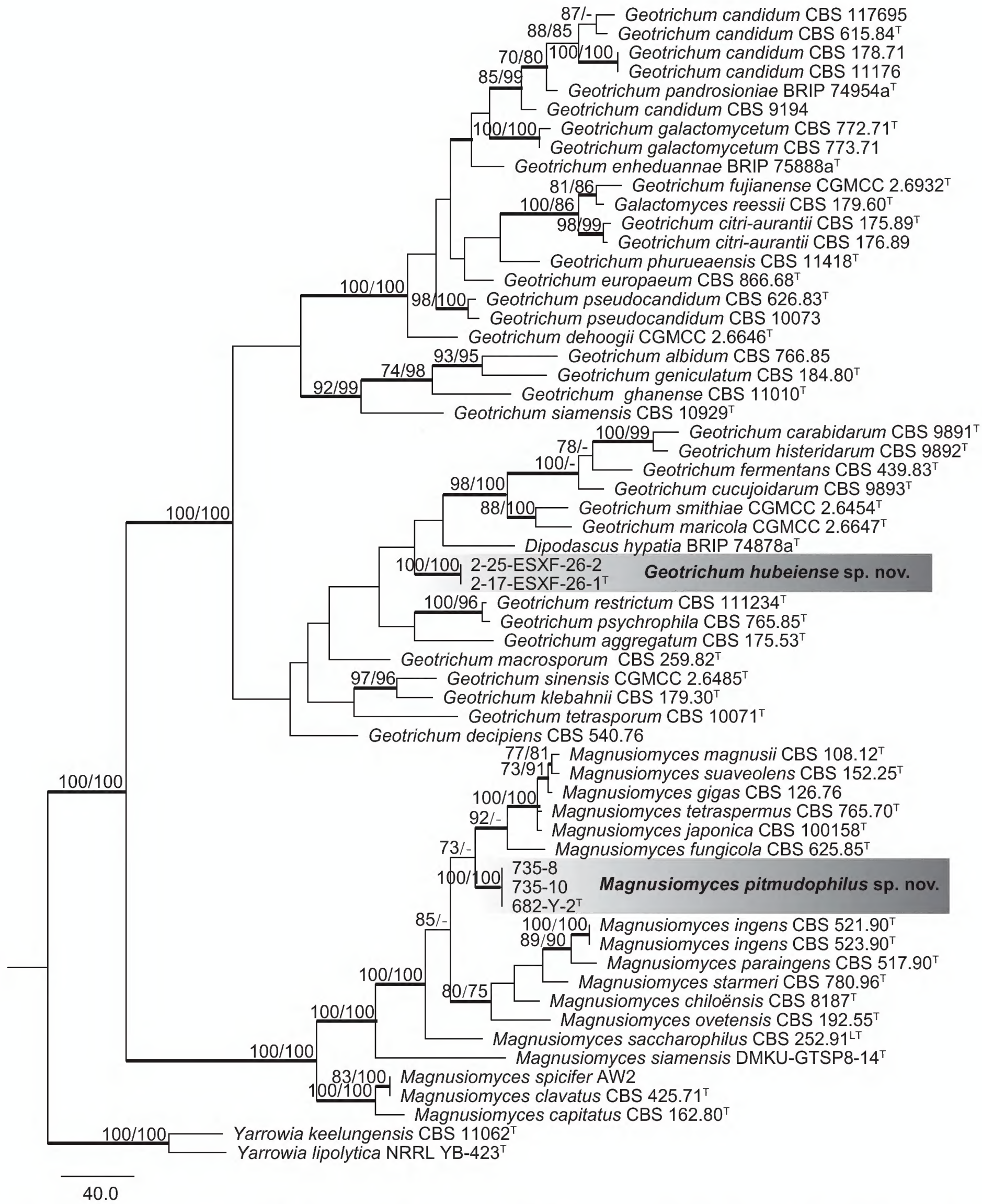

Figure 1. Phylogeny of arthroconidial yeast species based on maximum parsimony (MP) analysis of the combined ITS and D1/D2 sequences. The two *Yarrowia* species were used as the outgroup. The MP/maximum likelihood (ML) bootstrap support values equal to or above 70% are shown. Bold lines represent posterior probabilities equal to or above 0.95 from the Bayesian Inference (BI) test. Type strains are marked with the superscript "T". Lectotype strain is marked with the superscript "LT".

species *M. saccharophilus* were not resolved when the combined ITS and D1/D2 sequences and single ITS or D1/D2 sequences were used (Fig. 1, Suppl. material 1, 2). The group 682-Y-2^{T} differed from the type strains of the described

Table 1. Sequence differences between *M. pitmudophilus* sp. nov. and the type strains of the closely related species.

Species	D1/D2 domain		ITS region	
	Difference (%)	Substitutions/gaps/ total length	Difference (%)	Substitutions/gaps/ total length
M. fungicola	2.8	10/1/400	7.5	13/7/265
M. gigas	2.5	10/0/399	5.5	9/5/254
M. japonica	2.2	8/1/400	5.5	10/4/253
M. magnusii	2.0	8/0/399	5.5	9/5/254
M. saccharophilus	4.5	18/0/399	7.6	14/5/249
M. suaveolens	2.5	10/0/399	5.9	8/7/256
M. tetraspermus	3.5	14/0/399	6.3	11/5/254

species in the branch, including the seven species, by 8 to 18 (2.0–4.5%) nucleotide differences and 14 to 20 (5.5–7.6%) nucleotide differences in the D1/D2 domain and ITS region, respectively (Table 1). These results suggested that the three strains represent a novel species in the *Magnusiomyces* genus, for which *M. pitmudophilus* is proposed.

Taxonomy

Geotrichum hubeiense **L.C. Guo, H.Y. Zhu, P.J. Han & F.Y. Bai, sp. nov.**
Fungal Names: FN 572209
Fig. 2

Etymology. The species is named after the location "Hubei Province, China," where the type strain of the species was collected.

Holotype. CHINA • Hubei Province, Enshi City, Xianfeng County, from a bark sample, on July 7, 2023, L.C. Guo, (holotype CGMCC 2.7499^{T}, permanently preserved in a metabolically inactive state, ex-holotype JCM 36896 = 2-17-ESXF-26-1).

Description. ***Culture characteristics*****:** After 10 days on YPD agar at 30 °C, colonies are 22 mm in diameter, flesh colour, flat, dry, with finely hairy and regular margins (Fig. 2A). Hyphae soon disarticulate into cubic arthroconidia measuring 2.1–5.2 × 3.8–9.8 μm (Fig. 2B–C). Hyphae and arthroconidia produce oblong blastoconidia measuring 2.9–6.8 × 5.2–17.2 μm, which were observed on PDA and YCB agar after one month at 25 °C (Fig. 2D). Sexual structures were not observed on YCB, PDA, V8, YM, and CMA agar. ***Physiological and biochemical characteristics*****:** Glucose is not fermented. Glucose, D-galactose, L-sorbose, D-xylose, ethanol, glycerol, D-mannitol, D-glucitol, DL-lactic acid, succinic acid (weak), and citric acid (weak) are assimilated as sole carbon sources. Trehalose, ribitol, sucrose, D-maltose, cellobiose (slow), lactose, melibiose, raffinose, melezitose, inulin, starch soluble, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, erythritol, galactitol, α-methyl-D-glucoside, salicin, D-glucuronic acid, inositol, hexadecane, N-acetyl-D-glucosamine, and xylitol are not assimilated as sole carbon sources. Ethylamine, cadaverine, ammonium sulfate, L-lysine, potassium nitrate (late), and sodium nitrite (weak) are assimilated as sole nitrogen sources. Urease activity is negative. Diazonium Blue B reaction is negative. Extracellular starch compounds are not produced. No growth occurs in 10% (w/v) sodium chloride plus 5% (w/v) glucose medium. Growth occurs on 60% (w/v) glucose-yeast extract agar. Growth in vitamin-free medium is positive. Growth occurs on YPD agar at 35 °C, but not at 37 °C.

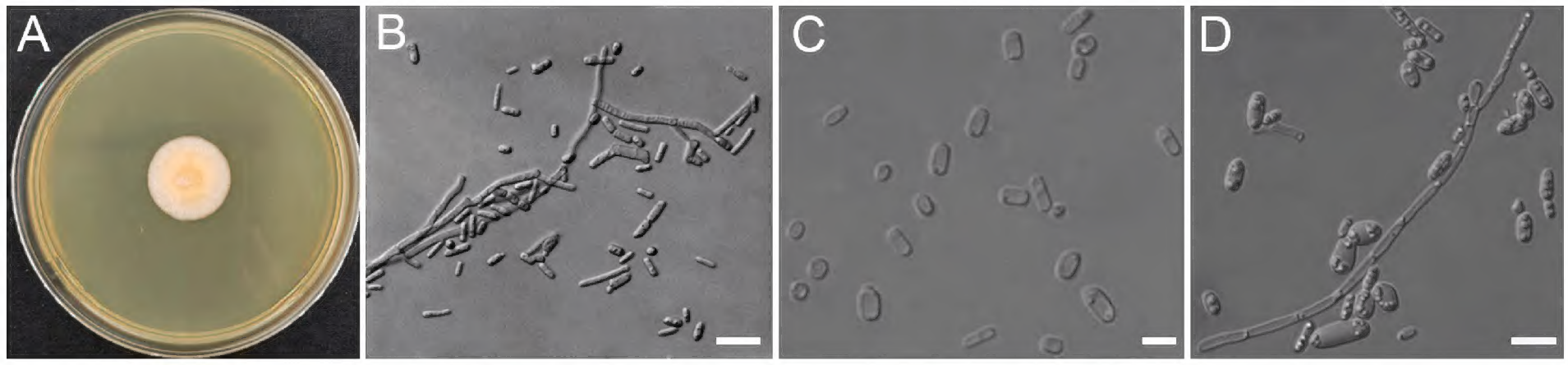

Figure 2. Morphology of *G. hubeiense* sp. nov. (Strain CGMCC 2.7499[T]) **A** colonies on yeast extract peptone dextrose (YPD) after 10 days **B** cylindrical arthroconidia on yeast extract–malt extract (YM) **C** cylindrical arthroconidia on V8 agar **D** blastoconidia on potato dextrose agar (PDA). Scale bars: 10 μm (**B–D**).

Materials examined. China • Hubei Province, Enshi City, Xianfeng County, from a bark sample, in July 2023, L.C. Guo, living culture 2-25-ESXF-26-2 = CGMCC 2.7418 = JCM 36897.

Notes. Physiologically, *G. hubeiense* sp. nov. differs from its closely related species, *G. carabidarum* and *G. histeridarum*, in its ability to assimilate D-galactose and grow on 60% (w/v) glucose-yeast extract agar.

Magnusiomyces pitmudophilus **Y.H. Wei, H.Y. Zhu, P.J. Han & F.Y. Bai, sp. nov.**
Fungal Names: FN 572210
Fig. 3

Etymology. The species is named after the isolation source, pit mud.

Holotype. China • Guizhou Province, Zunyi City, Xishui County, from a pit mud sample, on May 8, 2023, X.L. You and E.D. Fan, (holotype CGMCC 2.7496[T] permanently preserved in a metabolically inactive state, ex-holotype JCM 36982 = 682-Y-2).

Description. ***Culture characteristics*****:** After 10 days on YPD agar at 30 °C, colonies are 28 mm in diameter, white, dry, and powdery, with finely hairy and irregular margins (Fig. 3A). Hyphae soon disarticulate into cubic arthroconidia measuring 3.3–7.7 × 8.1–29.0 μm (Fig. 3B–C). Hyphae and arthroconidia produce oblong blastoconidia measuring 5.3–8.3 × 7.2–15.2 μm on PDA agar after one month at 25 °C (Fig. 3D). Sexual structures were not observed on YCB, PDA, V8, YM, and CMA agar. ***Physiological and biochemical characteristics*****:** Glucose is not fermented. Glucose, D-galactose, L-sorbose, ethanol, glycerol, D-glucitol, D-mannitol, and DL-lactic acid (weak) are assimilated as sole carbon sources. Trehalose, ribitol, succinic acid, citric acid, sucrose, D-maltose, cellobiose, lactose, melibiose, raffinose, melezitose, inulin, starch soluble, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, erythritol, galactitol, α-methyl-D-glucoside, salicin, D-glucuronic acid, inositol, hexadecane, N-acetyl-D-glucosamine, and xylitol are not assimilated as sole carbon sources. Ethylamine, cadaverine, ammonium sulfate, L-lysine, potassium nitrate (weak), and sodium nitrite (weak) are assimilated as sole nitrogen sources. Urease activity is positive. Diazonium Blue B reaction is negative. Extracellular starch compounds are not produced. No growth occurs in 10% (w/v) sodium chloride plus 5% (w/v) glucose medium. Growth occurs on 50% (w/v) glucose-yeast extract agar. No growth occurs on 60% (w/v) glucose-yeast

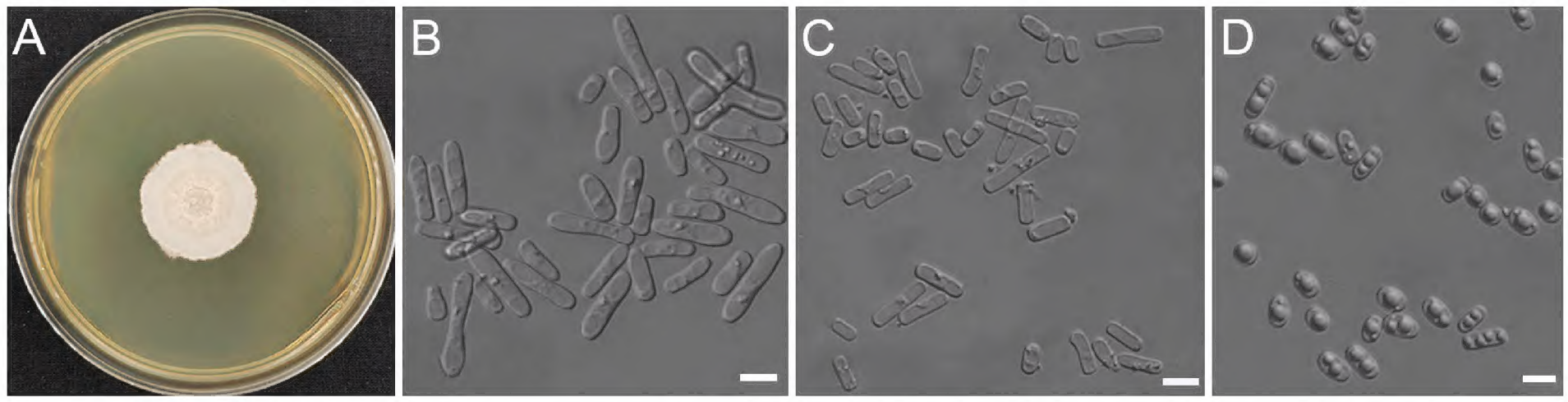

Figure 3. Morphology of *M. pitmudophilus* sp. nov. (Strain CGMCC 2.7496[T]) **A** colonies on yeast extract peptone dextrose (YPD) after 10 days **B** cylindrical arthroconidia on yeast extract–malt extract (YM) **C** cylindrical arthroconidia on V8 agar **D** blastoconidia on potato dextrose agar (PDA). Scale bars: 10 μm (**B–D**).

Table 2. Salient phenotypical characteristics distinguishing *M. pitmudophilus* sp. nov. from the closely related species. NA: not available.

Species	Fermentation			Assimilation	Growth		
	Glucose	Galactose	Sucrose	Succinate	35 °C	37 °C	40 °C
M. pitmudophilus sp. nov.	–	–	–	–	+	–	–
M. fungicola	–	–	–	+	+	w	–
M. gigas	+	+	–	+	+	–	–
M. japonica	NA	NA	NA	+	+	–	–
M. magnusii	+	+/w	+	+	–	–	–
M. saccharophilus	+	v	–	+/w	+	–	–
M. suaveolens	+	v	–	+/w	+	–	–
M. tetraspermus	+	–	–	+	+	+	+

extract agar. Growth in vitamin-free medium is positive. Growth occurs on YPD agar at 35 °C, but not at 37 °C.

Materials examined. China • Guizhou Province, Zunyi City, Xishui County, a pit mud sample, on May 8, 2023, X.L. You and E.D. Fan, living culture 735-8 = CGMCC 2.7774 = JCM 36984; • *ibid*. living culture 735-10 = CGMCC 2.7775.

Notes. Physiologically, *M. pitmudophilus* sp. nov. differs from its closely related species *M. fungicola* and *M. japonica* in its inability to assimilate succinic acid, from *M. suaveolens* and *M. saccharophilus* in its inability to ferment glucose, from *M. gigas* in its inability to ferment both glucose and galactose, from *M. magnusii* in its inability to ferment glucose, galactose, and sucrose, and from *M. tetraspermus* in its inability to ferment glucose and grow at 37 °C (Table 2). The three strains representing *M. pitmudophilus* sp. nov. are from pit mud collected in China, suggesting the unique niche of the new species.

Discussion

In this study, two novel species, *Geotrichum hubeiense* and *Magnusiomyces pitmudophilus*, were recognized based on ITS and D1/D2 sequence analyses. Currently, 30 *Geotrichum* species and 17 *Magnusiomyces* species have been accepted (Fig. 1, Suppl. material 3).

Arthroconidial yeast species are found globally in diverse environments, including wild and fermentation (Suppl. material 3). In the present study, we isolated the first novel species, *G. hubeiense*, from the bark in the Hubei Province of China. Other species, such as *Geotrichum albidum*, *G. klebahnii*,

G. macrosporum, *G. psychrophila*, *Magnusiomyces japonicus*, *M. quercus*, and *M. magnusii*, were all sourced from slime. *Geotrichum geniculatum* was isolated from guava, and *Geotrichum restrictum* from spruce (Suppl. material 3). They are all from plant-associated sources. The marine environment also hosts a variety of arthroconidial yeast species. Zhu et al. (2024b) described five *Geotrichum* species from marine habitats. *Geotrichum tetrasporum* was found in deep-sea sediments (de Hoog and Smith 2011b). Additionally, the guts of insects and soil are common sources for these species (Suppl. material 3). The diversity of these sources highlights the broad ecological adaptability of arthroconidial yeast species in various natural environments.

Meanwhile, we isolated the second novel species, *M. pitmudophilus*, and two known species, *Geotrichum candidum*, aligning with findings reported by Zhu et al. (2024b) and *Geotrichum europaeum*, both of which were extracted from the pit mud (data not shown). Pit mud offers a good medium for microbial growth and plays a significant role in the process of Chinese Baijiu brewing (Pan et al. 2023). In addition to the three species mentioned above, *Magnusiomyces ingens* and *Magnusiomyces paraingens* were also isolated from the wine cellar, an environment intrinsically linked to wine production (de Hoog and Smith 2011e). Beyond the fermentation milieu specific to wine, other distinct fermentation settings have been explored, such as the use of *Geotrichum ghanense* in the fermentation of cocoa (Nielsen et al. 2010) and *Geotrichum candidum* in dairy fermentation processes (Sulo et al. 2009; Groenewald et al. 2012). These results suggest that several arthroconidial yeast species occupy important ecological niches in the fermented environment and play crucial roles.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

Investigation: LCG, YHW, ZW, SH, XLY, EDF, SJY. Data curation: HYZ, YHW, LCG, SH, ZW. Methodology: HYZ, YHW. Molecular phylogeny: HYZ. Writing—original draft: HYZ, YHW. Writing—review and editing: DQW, FYB, PJH. All authors read and approved the final manuscript.

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Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

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Supplementary material 1

Phylogeny of the described arthroconidial yeast species based on neighbor-joining (NJ) analysis of the D1/D2 sequences

Authors: Hai-Yan Zhu, Yu-Hua Wei, Liang-Chen Guo, Zhang Wen, Shuang Hu, Di-Qiang Wang, Xiao-Long You, En-Di Fan, Shang-Jie Yao, Feng-Yan Bai, Pei-Jie Han

Data type: pdf

Explanation note: The two *Yarrowia* species were used as the outgroup. The NJ bootstrap support values equal to or above 70% are shown. Type strains are marked with the superscript “T”. Lectotype strain is marked with the superscript “LT”.

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Link: https://doi.org/10.3897/mycokeys.113.141799.suppl1

Supplementary material 2

Phylogeny of the arthroconidial yeast species based on neighbor-joining (NJ) analysis of the ITS sequences

Authors: Hai-Yan Zhu, Yu-Hua Wei, Liang-Chen Guo, Zhang Wen, Shuang Hu, Di-Qiang Wang, Xiao-Long You, En-Di Fan, Shang-Jie Yao, Feng-Yan Bai, Pei-Jie Han

Data type: pdf

Explanation note: The two *Yarrowia* species were used as the outgroup. The NJ bootstrap support values equal to or above 70% are shown. Type strains are marked with the superscript "T". Lectotype strain is marked with the superscript "LT".

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Supplementary material 3

The names, strain numbers, sources, locations, and corresponding GenBank accession numbers of the yeast taxa employed in this study

Authors: Hai-Yan Zhu, Yu-Hua Wei, Liang-Chen Guo, Zhang Wen, Shuang Hu, Di-Qiang Wang, Xiao-Long You, En-Di Fan, Shang-Jie Yao, Feng-Yan Bai, Pei-Jie Han

Data type: xls

Explanation note: All the new isolates used in this study are indicated in bold. Superscript T: Type strain. Superscript LT: Lectotype strain. Superscript IT: Isotype strain. *: Sequences obtained from the genome.

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